

Hands On : Using MaBoSS with WebMaBoSS

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Computational Systems Biology for Complex Human Disease
from static to dynamic representations of disease mechanisms

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WebMaBoSS

A web tool for simulating Boolean models

Click [here](#) to login if you already have an account, otherwise you can quickly create one [here](#).

If you want to quickly test WebMaBoSS, you can have a look at our [demo project](#).

Model analysis

WebMaBoSS allows simulations, and multiple outputs for results. It also allows sensitivity analysis by performing single and double mutations.

Compatibility

WebMaBoSS is able to import models in MaBoSS format (bnd, cfg files), BoolNet format, SBML-qual format, or in GINsim format. It also allows to export models in any of these three formats.

Public databases


WebMaBoSS allows to browse models from CellCollective and BioModels, and import them.

WebMaBoSS was created and is maintained by the team [Computational System Biology of Cancer](#) at [Institut Curie](#).

It is open-source and available on [GitHub](#), where you can also find instructions to run it locally and tutorials.

› Create an account

Register to WebMaBoSS



Username

E-mail (optional)

Password

Confirm password

[Register](#)

> Logging in

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Demo [Sign in](#) [Register](#)

Sign in



Username

Password

[Sign in](#)

> List of projects

Projects

Name

Cell Cycle



Metastasis



Cell Fate



Tutorial



Cancer models



New project

› Creating a project

The screenshot shows the 'WebMaBoSS' application interface. At the top, there is a navigation bar with 'WebMaBoSS', 'Tutorials', and 'About' on the left, and 'Profile' and 'Logout' on the right. The main content area is titled 'Projects'. On the left side of this area, there is a list of project categories: 'Name', 'Cell Cycle', 'Metastasis', 'Cell Fate', 'Tutorial', and 'Cancer models'. Below this list is a 'New project' button. In the center, a modal dialog box titled 'Add new project' is open. It contains two input fields: 'Name' with the text 'Invasion models' and 'Description' with the text 'Models describing invasion'. At the bottom of the dialog are two buttons: 'Close' (red) and 'Create project' (blue). On the right side of the 'Projects' section, there is a table with five rows, each containing a blue edit icon and a red delete icon.

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Projects

Name

Cell Cycle

Metastasis

Cell Fate

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New project

Add new project

Name

Invasion models

Description

Models describing invasion

Close Create project

> List of models

Models

Name

Montagud 2021 Prostate Cancer



Load model

Import model

› Loading a model

The screenshot shows the 'Load model' dialog box in the WebMaBoSS application. The background is a dimmed view of the 'Models' page, which includes a table with one entry: 'Montagud 2021 Prostate Cancer'. The dialog box is a light gray modal with a title bar 'Load model'. It contains the following fields and controls:

- Name:** A text input field containing 'Cohen 2015 Invasion model'.
- Type:** A dropdown menu currently showing 'MaBoSS'.
- BND file:** A text input field containing 'metastasis.bnd' and a 'Browse' button to its right.
- CFG file:** A text input field containing 'metastasis.cfg' and a 'Browse' button to its right.
- Buttons:** At the bottom of the dialog, there is a red 'Close' button on the left and a blue 'Load model' button on the right.

› Importing a model

WebMaBoSS Models Tutorials About

Models

Name

Montagud 2021 Pro

Load model Imp

Import model

Profile Logout

Import model

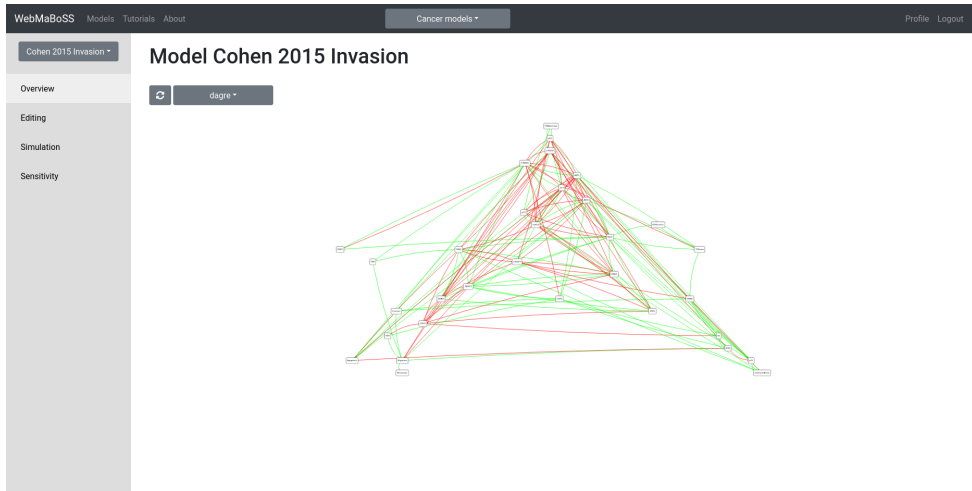
BioModels CellCollective

Name	Author
Traynard2016 - Mammalian cell cycle regulation - Logical Model	Pauline Traynard
Cacace2020 - Logical model of the regulatory network controlling...	Denis Thieffry
Howell2020- Compartmental Logical model of mitotic exit	Rowan Howell
Terfve2012 - Signalling in liver cancer - logical model	Vijayalakshmi Chelliah
Floc'hay2020 - SeaUrchin_model_ginsim	Denis Thieffry
Mbodj2016 - Mesoderm specification during Drosophila develop...	Denis Thieffry
Rodriguez-Jorge2019 - Boolean model of TCR signaling for CD4 +...	Denis Thieffry
Rodriguez-Jorge2019 - Boolean model of combined TCR and TLR...	Denis Thieffry
Afenya2018 - peripheral blood dynamics in the disease state	Szeyi Ng

☒ Use SBML names

Close

› Model interaction graph



› Creating a new simulation : General settings

The screenshot displays the WebMaBoSS web application interface. At the top, a navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', and 'About' on the left, and 'Profile' and 'Logout' on the right. A sidebar on the left contains a dropdown menu for 'Cohen 2015 Invasion' and a list of options: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area shows the title 'Model Cohen 2015 Invasion' and a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open, featuring four tabs: 'General' (selected), 'Initial states', 'Output', and 'Mutations'. The 'General' tab contains the following fields and controls:

- Name:** A text input field with the placeholder 'Name of the simulation'.
- Max time:** A numeric input field with the value '40' and a spinner icon.
- Sample count:** A numeric input field with the value '1000' and a spinner icon.
- Discrete time:** A toggle switch currently turned off.
- Use physical random generator:** A toggle switch currently turned off.
- Pseudorandom seed:** A numeric input field with the value '0' and a spinner icon.

At the bottom of the dialog box, there is a red 'Close' button on the left and a 'Submit' button on the right.

› Creating a new simulation : Initial states

The screenshot shows the WebMaBoSS web interface. A modal dialog titled 'Create new simulation' is open, displaying the 'Initial states' tab. The dialog lists several biological parameters with sliders and percentage values:

Parameter	Value
CTNNB1	0 %
CellCycleArrest	0 %
DKK1	0 %
DNADamage	50 %
ECMicroenv	50 %
EMT	0 %

At the bottom of the dialog, there are two buttons: 'Close' (in a red box) and 'Submit'.

› Creating a new simulation : Output nodes

The screenshot displays the WebMaBoSS web interface. At the top, there is a navigation bar with links for 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. On the left side, a sidebar menu lists 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and includes a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open, featuring four tabs: 'General', 'Initial states', 'Output', and 'Mutations'. The 'Output' tab is currently selected, showing a list of nodes with toggle switches: AKT1 (off), AKT2 (off), Apoptosis (on), CDH1 (off), CDH2 (off), CTNNB1 (off), and CellCycleArrest (on). At the bottom of the dialog, there are 'Close' and 'Submit' buttons.

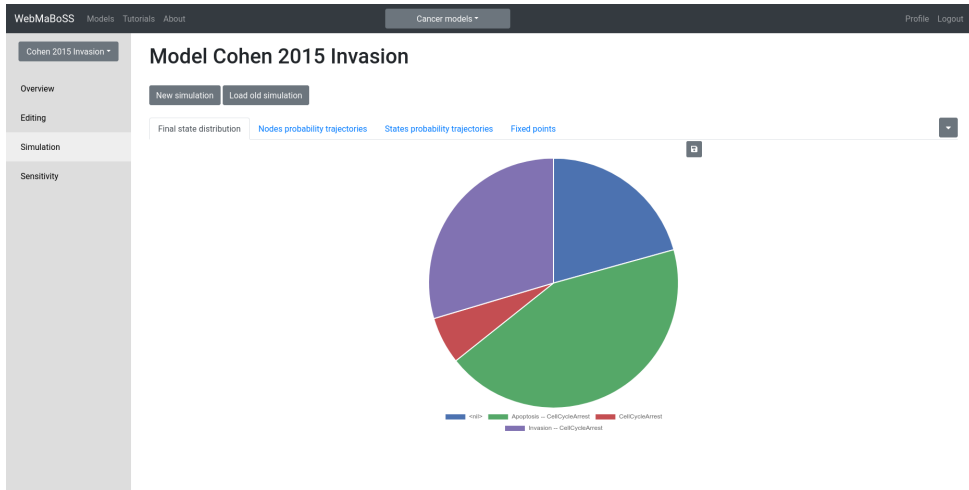
Node	Status
AKT1	Off
AKT2	Off
Apoptosis	On
CDH1	Off
CDH2	Off
CTNNB1	Off
CellCycleArrest	On

› Creating a new simulation : Mutants

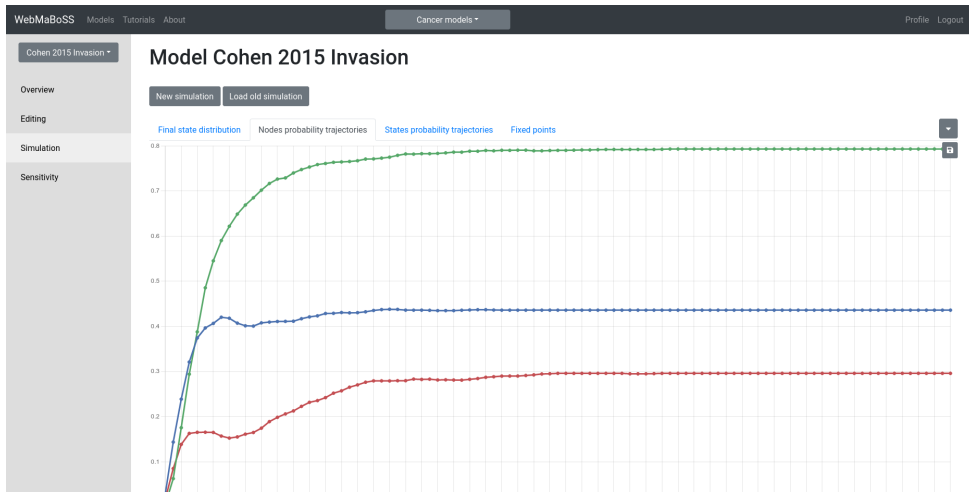
The screenshot displays the WebMaBoSS web application interface. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. The left sidebar contains a dropdown menu for 'Cohen 2015 Invasion' and a list of options: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area shows the title 'Model Cohen 2015 Invasion' and a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open, featuring four tabs: 'General', 'Initial states', 'Output', and 'Mutations'. The 'Mutations' tab is active, showing a list of genetic elements with toggle switches: AKT1 (enabled), AKT2 (disabled), Apoptosis (disabled), CDH1 (disabled), CDH2 (disabled), CTNNB1 (disabled), and CellProlifArrest (disabled). At the bottom of the dialog are 'Close' and 'Submit' buttons.

Element	Status
AKT1	Enabled
AKT2	Disabled
Apoptosis	Disabled
CDH1	Disabled
CDH2	Disabled
CTNNB1	Disabled
CellProlifArrest	Disabled

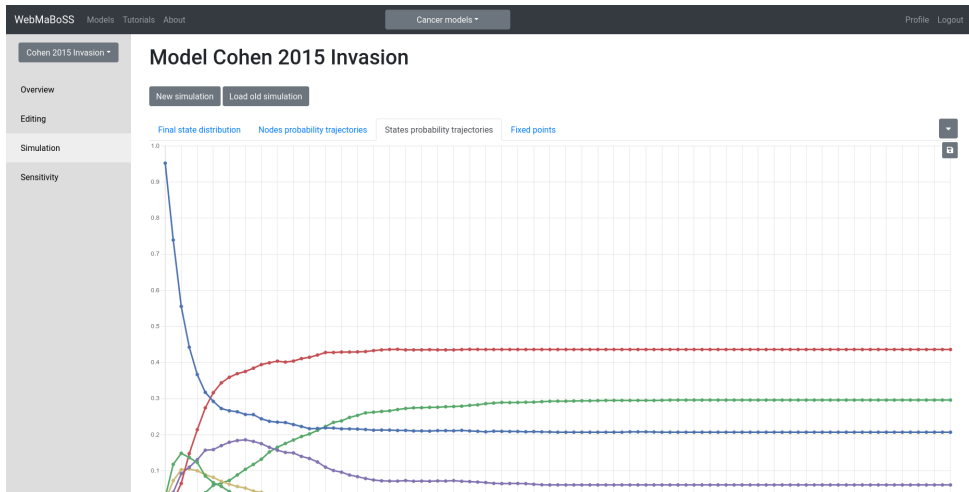
Simulation results : Final states



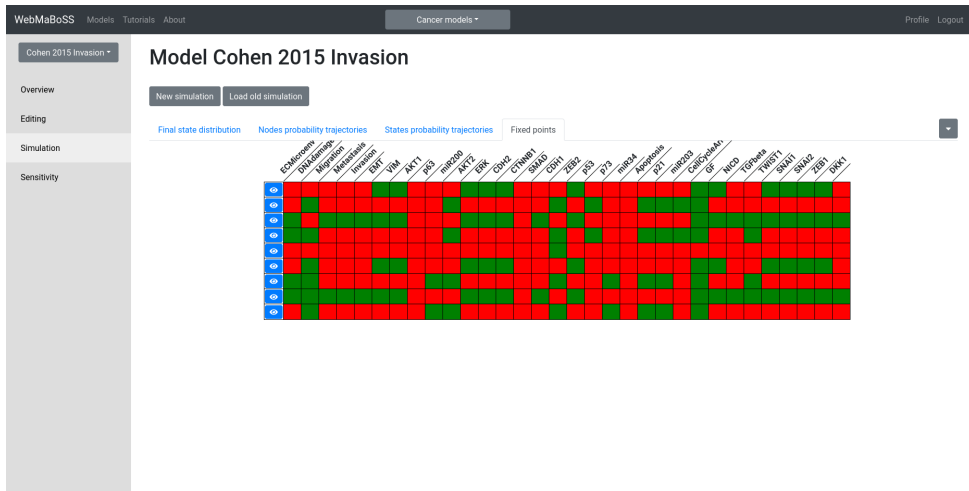
Simulation results : Node trajectories



› Simulation results : State trajectories



Simulation results : Fixed points



- Model editing : (in)activation rules

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Rates

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Parameters

Settings

AKT1			
AKT2			
Apoptosis			
CDH1			
CDH2			
CTNNB1			
CellCycleArrest			
rateUp	@logic ? \$u_CellCycleArrest : 0		
rateDown	@logic ? 0 : \$d_CellCycleArrest		
logic	((p21 & IZEB2 & IAKT1 & ImlR200 & ImlR203 & miR34) (p21 & IZEB2 & IAKT1 & ImlR200 & miR203) (p21 & IZEB2 & IAKT1 & miR200) (p21 & ZEB2 & IAKT1) (p21 & IAKT1))		
DDK1			
DNA Damage			
ECMicroenv			
EMT			
ERK			
GF			
Invasion			
Metastasis			
Migration			
NICD			
SMAD			
SNAI1			

› Model editing : (in)activation rules

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Cohen 2015 Invasion

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Model Cohen 2015 Invasion

Rates Initial values Outputs Parameters

AKT1

AKT2

Apoptosis

CDH1

CDH2

CTNNB1

CellCycleArrest

rateUp @logic ? \$u_CellCycleArrest : 0

rateDown @logic ? 0 : \$d_CellCycleArrest

logic (lp21 & lZEB2 & lAKT1 & lmiR200 & lmiR203 & miR34) | (lp21 & lZEB2 & lAKT1 & lmiR200 & miR203) | (lp21 & lZEB2 & lAKT1 & miR200) | (lp21 & lZEB2 & lAKT1) | (p21 & lAKT1)

DKK1

DNA damage

ECMicroenv

EMT

ERK

GF

Invasion

Metastasis

Migration

NICD

SMAD

SNAI1

Editing formula

Name

logic

Formula

(lp21 & lZEB2 & lAKT1 & lmiR200 & lmiR203 & miR34) | (lp21

Close Submit

> Model editing : Initial states

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	<input checked="" type="checkbox"/>	50%
AKT1	<input type="checkbox"/>	0%
AKT2	<input type="checkbox"/>	0%
Apoptosis	<input type="checkbox"/>	0%
CDH1	<input type="checkbox"/>	0%
CDH2	<input type="checkbox"/>	0%
CTNNB1	<input type="checkbox"/>	0%
CellCycleArrest	<input type="checkbox"/>	0%
DKK1	<input type="checkbox"/>	0%
DNA damage	<input checked="" type="checkbox"/>	50%
ECMicroenv	<input checked="" type="checkbox"/>	50%
EMT	<input type="checkbox"/>	0%
ERK	<input type="checkbox"/>	0%

› Model editing : Output nodes

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	<input type="checkbox"/>
AKT1	<input type="checkbox"/>
AKT2	<input type="checkbox"/>
Apoptosis	<input checked="" type="checkbox"/>
CDH1	<input type="checkbox"/>
CDH2	<input type="checkbox"/>
CTNNB1	<input type="checkbox"/>
CellCycleArrest	<input checked="" type="checkbox"/>
DKK1	<input type="checkbox"/>
DNA damage	<input type="checkbox"/>
ECMicroenv	<input type="checkbox"/>
EMT	<input type="checkbox"/>
ERK	<input type="checkbox"/>
GF	<input type="checkbox"/>
Invasion	<input checked="" type="checkbox"/>

› Model editing : Parameters

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Overview











































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RatesInitial valuesOutputsParametersSettings

\$d_AKT1	1		
\$d_AKT2	1		
\$d_Apoptosis	1		
\$d_CDH1	1		
\$d_CDH2	1		
\$d_CTNNB1	1		
\$d_CellCycleArrest	1		
\$d_DKK1	1		
\$d_DNA Damage	1		
\$d_ECMicroenv	1		
\$d_EMT	1		
\$d_ERK	1		
\$d_GF	1		
\$d_Invasion	1		
\$d_Metastasis	1		
\$d_Migration	1		
\$d_NICD	1		
\$d_SMAD	1		
\$d_SNAI1	1		
\$d_SNAI2	1		
\$d_TGFbeta	1		

› Model editing : Settings

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time_tick	0.5	
max_time	40	
sample_count	1000	
discrete_time	0	
use_physrandgen	0	
seed_pseudorandom	0	
display_traj	0	
statdist_traj_count	0	
statdist_cluster_threshold	1	
thread_count	6	
statdist_similarity_cache_max_size	20000	

› Sensitivity analysis : General settings

The screenshot displays the WebMaBoSS web application interface. At the top, a dark navigation bar contains the logo 'WebMaBoSS' and links for 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. On the left, a sidebar menu lists 'Cohen 2015 Invasion', 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and features a 'New sensitivity analysis' button. A modal dialog box titled 'New sensitivity analysis' is open, showing three tabs: 'General' (selected), 'Candidates', and 'Output'. The 'General' tab contains a 'Name' input field with the placeholder 'Name of the simulation', two toggle switches for 'Single mutations' and 'Double mutations' (both currently off), and a 'Local' dropdown menu. At the bottom of the dialog are 'Close' and 'Submit' buttons.

› Sensitivity analysis : Mutant candidates

The screenshot displays the WebMaBoSS web application interface. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', and user links 'Profile' and 'Logout'. The left sidebar contains a dropdown menu for 'Cohen 2015 Invasion' and a list of options: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and features a 'New sensitivity analysis' button. A modal window titled 'New sensitivity analysis' is open, showing three tabs: 'General', 'Candidates', and 'Output'. The 'Candidates' tab is active, displaying a list of biological processes with toggle switches: ERK (on), GF (on), Invasion (off), Metastasis (off), Migration (off), and NICD (on). At the bottom of the modal are 'Close' and 'Submit' buttons.

Process	Status
ERK	On
GF	On
Invasion	Off
Metastasis	Off
Migration	Off
NICD	On

› Sensitivity analysis : Output nodes

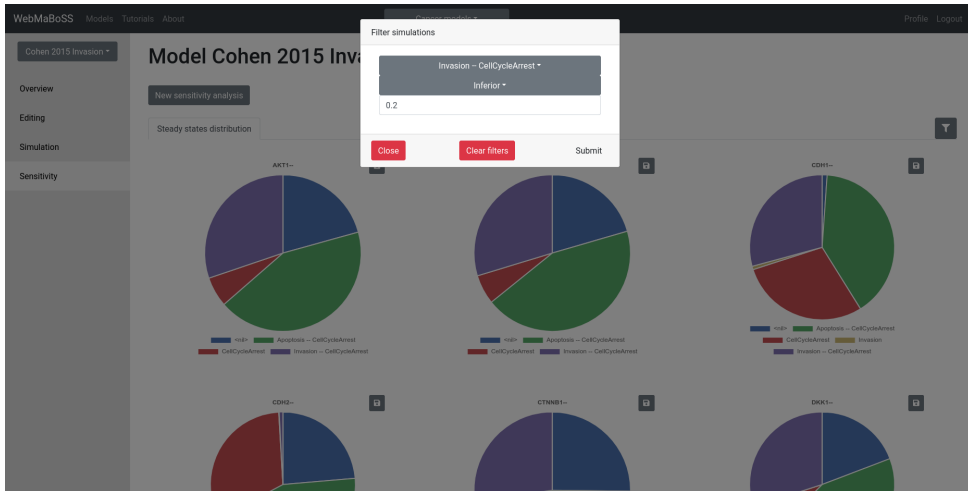
The screenshot displays the WebMaBoSS web application interface. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. The left sidebar shows a menu with 'Cohen 2015 Invasion' selected, and sub-items: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and contains a 'New sensitivity analysis' button. A modal dialog box titled 'New sensitivity analysis' is open, showing three tabs: 'General', 'Candidates', and 'Output'. The 'Output' tab is active, displaying a list of nodes with toggle switches: AKT1, AKT2, Apoptosis (checked), CDH1, CDH2, and CTNNB1. At the bottom of the dialog are 'Close' and 'Submit' buttons.

Node	Toggle State
AKT1	Off
AKT2	Off
Apoptosis	On
CDH1	Off
CDH2	Off
CTNNB1	Off

> Sensitivity analysis : Results



› Sensitivity analysis : Filtering results



› Sensitivity analysis : Filtered results



- › Hands on

- › Create a new project
- › Load Cohen's model (bnd and cfg available in google drive)
- › Perform default simulation, report CellCycleArrest state final percentage
- › Perform simulation with ECMicroenv and DNADamage on, report Apoptosis node final percentage
- › Perform simulation with NICD++, p53– mutant, report number of fixed points

- › Hands on

- › Perform sensitivity analysis on single mutants, testing only inhibitions
- › Filter mutants where state Invasion – CellCycleArrest is less than 20%
- › Report mutants found with such phenotypes